

09/831142

JC08 Rec'd PCT/PTO 07 MAY 2001

PATENTS

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Anthony Keith CAMPBELL

Serial No.

Filed herewith

PROTEIN AND DNA CODING THEREFOR

**SUBMISSION UNDER 37 C.F.R. §821
FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE
SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

Assistant Commissioner for Patents

Washington, D.C. 20231

Sir:

Applicant attach to the present paper a "Sequence Listing", as required by Rule 821(c), and a copy of the "Sequence Listing" in computer readable form, as required by Rule 821(e).

Applicant hereby states that the content of the attached paper and computer readable copy of the Sequence Listing are the same.

Respectfully submitted,

YOUNG & THOMPSON

By

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Arlington, VA 22202
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May 7, 2001

SEQUENCE LISTING

<110> CAMPBELL, ANTHONY KEITH

<120> PROTEIN AND DNA CODING THEREFOR

<130> WCM.69.US

<140> 09/831,142

<141> 2001-05-07

<150> PCT/GB99/03654

<151> 1999-11-05

<150> GB 9824357.9

<151> 1998-11-07

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 870

<212> DNA

<213> Pholas dactylus

<220>

<221> CDS

<222> (30)..(704)

<400> 1

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| | | | Met | Ala | Cys | Ile | Val | Phe | Val | Ala | |
| | | | 1 | | | | | | 5 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ctt | gtc | gct | cta | tgc | tta | atg | caa | ccg | ggt | tcc | ggt | gag | gaa | gta | caa | 101 |
| Leu | Val | Ala | Leu | Cys | Leu | Met | Gln | Pro | Gly | Ser | Gly | Glu | Glu | Val | Gln | |
| 10 | | | | | | 15 | | | | | 20 | | | | | |

| | | | | | | | | | | | | | | | |
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| tgc | gct | aat | tgg | aca | caa | gct | aat | gaa | tat | gtg | ttc | aac | gtg | gac | 149 |
| Cys | Ala | Met | Asn | Trp | Thr | Gln | Ala | Asn | Glu | Tyr | Val | Phe | Asn | Val | Asp |
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| tgg | atg | acc | att | ttc | atc | tac | gac | tat | ggc | gct | caa | gag | caa | ctg | tac | 197 |
| Trp | Met | Thr | Ile | Phe | Ile | Tyr | Asp | Tyr | Gly | Ala | Gln | Glu | Gln | Leu | Tyr | |
| | | | | | | 45 | | | 50 | | | | 55 | | | |

| | | | | | | | | | | | | | | | | |
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| gaa | gat | cgg | gct | ttg | ggg | ctg | tgt | cgg | att | gaa | cgg | gcc | ggc | cca | ggt | 245 |
| Glu | Asp | Arg | Ala | Leu | Gly | Leu | Cys | Arg | Ile | Glu | Arg | Ala | Gly | Pro | Gly | |
| 60 | | | | | | | | | 65 | | | | 70 | | | |

| | | | | | | | | | | | | | | | | |
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| acc | aca | aaa | gcc | gtc | tgg | att | aac | tgg | agt | aac | gac | acg | cag | tca | tgt | 293 |
| Thr | Thr | Lys | Ala | Val | Trp | Ile | Asn | Trp | Ser | Asn | Asp | Thr | Gln | Ser | Cys | |
| 75 | | | | | | | 80 | | | | | 85 | | | | |

| | | | | | | | | | | | | | | | | |
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| gta | aca | aga | aaa | aca | atc | ttc | ttc | gag | gtt | ggt | gga | gaa | att | gcc | cgg | 341 |
| Val | Thr | Arg | Lys | Thr | Ile | Phe | Phe | Glu | Val | Gly | Gly | Glu | Ile | Ala | Arg | |
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| ctt gtt gac tac aga cca cag gaa gac gga act gag aaa act ttt aca Leu Val Asp Tyr Arg Pro Gln Glu Asp Gly Thr Glu Lys Thr Phe Thr 105 110 115 120 | 389 |
| aga aaa ttc tct agc aaa atg cca ggc act tac atg ctt atg gac gtg Arg Lys Phe Ser Ser Lys Met Pro Gly Thr Tyr Met Leu Met Asp Val 125 130 135 | 437 |
| tgc gct aca agg gac gct gat gat aaa tgc atc gaa ggc aca att gtg Cys Ala Thr Arg Asp Ala Asp Asp Lys Cys Ile Glu Gly Thr Ile Val 140 145 150 | 485 |
| gtg aca gtc agg gtg tcc cta tat gac gaa gat aac aat ggt gta atg Val Thr Val Arg Val Ser Leu Tyr Asp Glu Asp Asn Asn Gly Val Met 155 160 165 | 533 |
| gat gaa ggt aag gtg att cca tct gag aca atc gag gat gat atc aag Asp Glu Gly Lys Val Ile Pro Ser Glu Thr Ile Glu Asp Asp Ile Lys 170 175 180 | 581 |
| gac tgt ggg ctc tta gac caa gat gtt gaa ctc gat tat acg tgg act Asp Cys Gly Leu Leu Asp Gln Asp Val Glu Leu Asp Tyr Thr Trp Thr 185 190 195 200 | 629 |
| caa aac gag tgt gat cta cca gac aca gta gac gag gct gaa gac aca Gln Asn Glu Cys Asp Leu Pro Asp Thr Val Asp Glu Ala Glu Asp Thr 205 210 215 | 677 |
| ccg tca gaa act gga gaa ttc ttc tgg tagatctatc agactactt Pro Ser Glu Thr Gly Glu Phe Trp 220 225 | 724 |
| tatcagcagg acaactggtc gttaccagac acctataacg tgcctcatc aataatgtgt aaaacagaaa taatcgatag aatattgaaa ataaaatgtt aataaacact ggttgaaata tgaaaaaaaaaaaaa ctcgag | 784 844 870 |
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<213> Pholas dactylus

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Asn Glu Tyr Val Phe Asn Val Asp Trp Met Thr Ile Phe Ile Tyr Asp
35 40 45

Tyr Gly Ala Gln Glu Gln Leu Tyr Glu Asp Arg Ala Leu Gly Leu Cys
50 55 60

Arg Ile Glu Arg Ala Gly Pro Gly Thr Thr Lys Ala Val Trp Ile Asn
65 70 75 80

Trp Ser Asn Asp Thr Gln Ser Cys Val Thr Arg Lys Thr Ile Phe Phe
85 90 95

Glu Val Gly Gly Glu Ile Ala Arg Leu Val Asp Tyr Arg Pro Gln Glu
100 105 110

Asp Gly Thr Glu Lys Thr Phe Thr Arg Lys Phe Ser Ser Lys Met Pro
115 120 125

Gly Thr Tyr Met Leu Met Asp Val Cys Ala Thr Arg Asp Ala Asp Asp
130 135 140

Lys Cys Ile Glu Gly Thr Ile Val Val Thr Val Arg Val Ser Leu Tyr
 145 150 155 160

Asp Glu Asp Asn Asn Gly Val Met Asp Glu Gly Lys Val Ile Pro Ser
 165 170 175

Glu Thr Ile Glu Asp Asp Ile Lys Asp Cys Gly Leu Leu Asp Gln Asp
 180 185 190

Val Glu Leu Asp Tyr Thr Trp Thr Gln Asn Glu Cys Asp Leu Pro Asp
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Thr Val Asp Glu Ala Glu Asp Thr Pro Ser Glu Thr Gly Glu Phe Phe
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Trp
 225

<210> 5
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 <212> PRT
 <213> Pholas dactylus

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Glu Gln Leu Tyr Glu Asp Arg Ala Leu Gly Leu Cys Arg Ile Glu Arg
 35 40 45

Ala Gly Pro Gly Thr Thr Lys Ala Val Trp Ile Asn Trp Ser Asn Asp
 50 55 60

Thr Gln Ser Cys Val Thr Arg Lys Thr Ile Phe Phe Glu Val Gly Gly
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Glu Ile Ala Arg Leu Val Asp Tyr Arg Pro Gln Glu Asp Gly Thr Glu
 85 90 95

Lys Thr Phe Thr Arg Lys Phe Ser Ser Lys Met Pro Gly Thr Tyr Met
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Leu Met Asp Val Cys Ala Thr Arg Asp Ala Asp Asp Lys Cys Ile Glu
 115 120 125

Gly Thr Ile Val Val Thr Val Arg Val Ser Leu Tyr Asp Glu Asp Asn
 130 135 140

Asn Gly Val Met Asp Glu Gly Lys Val Ile Pro Ser Glu Thr Ile Glu
 145 150 155 160

Asp Asp Ile Lys Asp Cys Gly Leu Leu Asp Gln Asp Val Glu Leu Asp
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Tyr Thr Trp Thr Gln Asn Glu Cys Asp Leu Pro Asp Thr Val Asp Glu
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Ala Glu Asp Thr Pro Ser Glu Thr Gly Glu Phe Phe Trp
 195 200 205

<210> 6
 <211> 225
 <212> PRT
 <213> Pholas dactylus

<400> 6
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 20 25 30

Asn Glu Tyr Val Phe Asn Val Asp Trp Met Thr Ile Phe Ile Tyr Asp
 35 40 45

Tyr Gly Ala Gln Glu Gln Leu Tyr Glu Asp Arg Ala Leu Gly Leu Cys
 50 55 60

Arg Ile Glu Arg Ala Gly Pro Gly Thr Thr Lys Ala Val Trp Ile Asn
 65 70 75 80

Trp Ser Asn Asp Thr Gln Ser Cys Val Thr Arg Lys Thr Ile Phe Phe
 85 90 95

Glu Val Gly Gly Glu Ile Ala Arg Leu Val Asp Tyr Arg Pro Gln Glu
 100 105 110

Asp Gly Thr Glu Lys Thr Phe Thr Arg Lys Phe Ser Ser Lys Met Pro
 115 120 125

Gly Thr Tyr Met Leu Met Asp Val Cys Ala Thr Arg Asp Ala Asp Asp
 130 135 140

Lys Cys Ile Glu Gly Thr Ile Val Val Thr Val Arg Val Ser Leu Tyr
 145 150 155 160

Asp Glu Asp Asn Asn Gly Val Met Asp Glu Gly Lys Val Ile Pro Ser
 165 170 175

Glu Thr Ile Glu Asp Asp Ile Lys Asp Cys Gly Leu Leu Asp Gln Asp
 180 185 190

Val Glu Leu Asp Tyr Thr Trp Thr Gln Asn Glu Cys Asp Leu Pro Asp
 195 200 205

Thr Val Asp Glu Ala Glu Asp Thr Pro Ser Glu Thr Gly Glu Phe Phe
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Trp
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17

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<223> A, T, C or G

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17

<210> 9
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<212> DNA
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<220>
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 <223> A, T, C or G

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<400> 10
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<210> 13
 <211> 24
 <212> DNA
 <213> Artificial sequence

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<400> 13
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<210> 14
<211> 19
<212> DNA
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oligonucleotide

<400> 14
caatttgtgcc ttcgatgca

19

<210> 15
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<220>
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oligonucleotide

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ggactgtggg ctcttag

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<210> 16
<211> 20
<212> DNA
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<220>
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oligonucleotide

<400> 16
atggcttcta tcgtttcgt

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<210> 17
<211> 27
<212> DNA
<213> Artificial sequence

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 aagagcaact gtacgaagat cgggcttgg ggctgtgtcg gattgaacgg gccggcccaag 180
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 aagacggAAC tgagaaaact ttacaagaa aattctctag caaaatgccca ggcacttaca 360
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 aggctgaaga cacaccgtca gaaactggag aattcttctg gtanatctat cagactactt 660
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 taaaac 726

<210> 24
 <211> 34
 <212> PRT
 <213> Saccharomyces cerevisiae

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Leu Pro Leu Glu Ser Leu Glu Leu Asp Gln Asp Val Glu Leu Asp Tyr
 20 25 30

Thr Trp

<210> 25
 <211> 31

<212> PRT
<213> Cyprinus carpio

<400> 25
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<210> 26
<211> 20
<212> PRT
<213> Synechocystis sp.

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Phe Asn Phe Asp
20

<210> 27
<211> 14
<212> PRT
<213> Emericella nidulans

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<213> Drosophila melanogaster

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<210> 29
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<213> Peptococcus niger

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<210> 30
<211> 25
<212> PRT
<213> Homo sapiens

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Asp Asp Leu Glu Asp Asp Ala Leu Asp
20 25

<210> 31
<211> 59
<212> PRT
<213> Vargula sp.

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Tyr Thr Glu Val Glu Lys Val Thr Ile Arg Lys Gln Ser Thr Val Val
20 25 30

Asp Leu Ile Val Asp Gly Lys Gln Val Lys Val Gly Gly Val Asp Val
35 40 45

Ser Ile Pro Tyr Ser Ser Glu Asn Thr Ser Ile
50 55

<210> 32
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<212> PRT
<213> Renilla sp.

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Gly Phe Leu Arg Val Ala Asp Gln Leu Gly Leu Ala Pro Gly Val Arg
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Ile Ser Val Glu Glu Ala Ala Val Asn Ala Thr Asp Ser Leu Leu Lys
35 40 45

Met Lys Ala Glu Glu Lys Ala Met Ala Val Ile Gln Ser Leu
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<210> 33
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative
P-loop binding motif

<400> 33
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1 5

<210> 34
<211> 4
<212> PRT
<213> Photinus pyralis

<400> 34
His His Gly Phe
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<220>
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illustrative peptide

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<210> 36
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Asp Lys Glu

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illustrative peptide

<400> 37
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<210> 38
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illustrative peptide

<400> 38
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<223> Description of Artificial Sequence: Synthetic
illustrative peptide

<400> 39
His Asp Glu Leu
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<210> 40
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<223> Description of Artificial Sequence: Synthetic
illustrative peptide

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illustrative peptide

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<210> 42
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<220>
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N-terminal acylation motif from Tyrosine kinase

<400> 42
Met Gly Cys Val Cys Ser Ser Asn Pro Asp
1 5 10

SEQUENCE LISTING

<110> University of Wales College of Medicine

<120> Protein and DNA coding therefor

<130> PCT/GB99/03654

<140> PCT/GB99/03654

<141> 1999-11-05

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 870

<212> DNA

<213> Pholas dactylus

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aagctaata gatatgtttc aacgtggact ggatgaccat tttcatctac gactatggcg 180
ctcaagagca actgtacgaa gatcgggctt tggggctgtg tcggattgaa cggccggcc 240
caggtaccac aaaagccgtc tggattaact ggagtaacga cacgcagtca tgtgtAACAA 300
gaaaaacaat ctcttcgag gtttgtggag aaattccccg gctagttgac tacagaccac 360
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tttgttgtac agtcagggtg tccctatatg acgaagataa caatggtgta atggatgaag 540
gtaaggtgat tccatctgag acaatcgagg atgatatcaa ggactgtggg ctcttagacc 600
aagatgttga actcgattat acgtggactc aaaacgagtg tgatctacca gacacagtag 660
acgaggctga agacacacccg tcagaaactg gagaattctt ctggtagatc tatcagacta 720
cttttatcag caggacaact ggtcggtacc agacacctat aacgtgtcct catcaataat 780
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gaggctgaag acacaccgtc agaaaactgga gaattcttct ggttagatcta tcagaccact 720
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atctgagaca atcgaggatg atatcaagga ctgtgggctc ttagaccaag atgttgaact 600
cgattatacg tggactcaaa acgagtgtga tctaccagac acagtagacg aggctgaaga 660
cacaccgtca gaaactggag aattcttctg gtagatctat cagaccactt ttatcagcag 720
gacaactggcgttaccaga cacctataac gtgtcctcat caataatgtg taaaacagaa 780
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Asn Glu Tyr Val Phe Asn Val Asp Trp Met Thr Ile Phe Ile Tyr Asp
35 40 45

Tyr Gly Ala Gln Glu Gln Leu Tyr Glu Asp Arg Ala Leu Gly Leu Cys
50 55 60

Arg Ile Glu Arg Ala Gly Pro Gly Thr Thr Lys Ala Val Trp Ile Asn

65 70 75 80

Trp Ser Asn Asp Thr Gln Ser Cys Val Thr Arg Lys Thr Ile Phe Phe
85 90 95

Glu Val Gly Gly Glu Ile Ala Arg Leu Val Asp Tyr Arg Pro Gln Glu
100 105 110

Asp Gly Thr Glu Lys Thr Phe Thr Arg Lys Phe Ser Ser Lys Met Pro
115 120 125

Gly Thr Tyr Met Leu Met Asp Val Cys Ala Thr Arg Asp Ala Asp Asp
130 135 140

Lys Cys Ile Glu Gly Thr Ile Val Val Thr Val Arg Val Ser Leu Tyr
145 150 155 160

Asp Glu Asp Asn Asn Gly Val Met Asp Glu Gly Lys Val Ile Pro Ser
165 170 175

Glu Thr Ile Glu Asp Asp Ile Lys Asp Cys Gly Leu Leu Asp Gln Asp
180 185 190

Val Glu Leu Asp Tyr Thr Trp Thr Gln Asn Glu Cys Asp Leu Pro Asp
195 200 205

Thr Val Asp Glu Ala Glu Asp Thr Pro Ser Glu Thr Gly Glu Phe Phe
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Trp
225

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Phe Asn Val Asp Trp Met Thr Ile Phe Ile Tyr Asp Tyr Gly Ala Gln
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Glu Gln Leu Tyr Glu Asp Arg Ala Leu Gly Leu Cys Arg Ile Glu Arg
35 40 45

Ala Gly Pro Gly Thr Thr Lys Ala Val Trp Ile Asn Trp Ser Asn Asp

50

55

60

Thr Gln Ser Cys Val Thr Arg Lys Thr Ile Phe Phe Glu Val Gly Gly
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Glu Ile Ala Arg Leu Val Asp Tyr Arg Pro Gln Glu Asp Gly Thr Glu
 85 90 95

Lys Thr Phe Thr Arg Lys Phe Ser Ser Lys Met Pro Gly Thr Tyr Met
 100 105 110

Leu Met Asp Val Cys Ala Thr Arg Asp Ala Asp Asp Lys Cys Ile Glu
 115 120 125

Gly Thr Ile Val Val Thr Val Arg Val Ser Leu Tyr Asp Glu Asp Asn
 130 135 140

Asn Gly Val Met Asp Glu Gly Lys Val Ile Pro Ser Glu Thr Ile Glu
 145 150 155 160

Asp Asp Ile Lys Asp Cys Gly Leu Leu Asp Gln Asp Val Glu Leu Asp
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Tyr Thr Trp Thr Gln Asn Glu Cys Asp Leu Pro Asp Thr Val Asp Glu
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Ala Glu Asp Thr Pro Ser Glu Thr Gly Glu Phe Phe Trp
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<400> 6

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Pro Gly Ser Gly Glu Glu Val Gln Cys Ala Met Asn Trp Thr Gln Ala
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Asn Glu Tyr Val Phe Asn Val Asp Trp Met Thr Ile Phe Ile Tyr Asp
 35 40 45

Tyr Gly Ala Gln Glu Gln Leu Tyr Glu Asp Arg Ala Leu Gly Leu Cys
 50 55 60

Arg Ile Glu Arg Ala Gly Pro Gly Thr Thr Lys Ala Val Trp Ile Asn

65 70 75 80

Trp Ser Asn Asp Thr Gln Ser Cys Val Thr Arg Lys Thr Ile Phe Phe
85 90 95

Glu Val Gly Gly Glu Ile Ala Arg Leu Val Asp Tyr Arg Pro Gln Glu
100 105 110

Asp Gly Thr Glu Lys Thr Phe Thr Arg Lys Phe Ser Ser Lys Met Pro
115 120 125

Gly Thr Tyr Met Leu Met Asp Val Cys Ala Thr Arg Asp Ala Asp Asp
130 135 140

Lys Cys Ile Glu Gly Thr Ile Val Val Thr Val Arg Val Ser Leu Tyr
145 150 155 160

Asp Glu Asp Asn Asn Gly Val Met Asp Glu Gly Lys Val Ile Pro Ser
165 170 175

Glu Thr Ile Glu Asp Asp Ile Lys Asp Cys Gly Leu Leu Asp Gln Asp
180 185 190

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Trp
225

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19

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<400> 15
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<210> 16
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<212> DNA
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| <210> 18 | | |
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| <400> 18 | | |
| ccacacggat ccttattgat gaggaca | | 27 |
| | | |
| <210> 19 | | |
| <211> 53 | | |
| <212> DNA | | |
| <213> Pholas dactylus | | |
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| <400> 19 | | |
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| | | |
| <210> 20 | | |
| <211> 54 | | |
| <212> DNA | | |
| <213> Pholas dactylus | | |
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| <400> 20 | | |
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| | | |
| <210> 21 | | |
| <211> 24 | | |
| <212> DNA | | |
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24

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20